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to 264 of CRAF1 (SEQ ID NO:8). (D) Zn finger from residues 45 to 106 of CRAF1 (SEQ ID NO:9). n, NH₂-terminus; c, COOH-terminus.

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Figures 5A-B. cDNA nucleotide sequence and predicted amino acid sequences of mouse CRAF1 (SEQ ID NO:4). The cDNA nucleotide sequence is also deposited in GenBank with accession number U21050.

Figures 6A-B. cDNA nucleotide sequence and predicted amino acid sequences of human CRAF1 (SEQ ID NO:5). The cDNA nucleotide sequence is also deposited in GenBank with accession number U21092.

A mark-up copy of the amendments to the Brief Description of the Figures is annexed hereto as **Exhibit B**.

In the Specification

Please amend the paragraph starting on page 11, line 10, as follows:

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- Variants within the scope of the invention include proteins and peptides with amino acid sequences having at least eighty percent homology with the COOH-terminal domain of CRAF1 (corresponding roughly to residues 415-567 (SEQ ID NO:12)) or with C26 (residues 324-567 of CRAF1 (SEQ ID NO:11)). More preferably the sequence homology is at least ninety percent, or at least ninety-five percent.
